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Reviewer: markspencer

Timestamp: [year=2008; month=10; day=24; hr=13; min=30; sec=35; ms=59; ]

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Application No: 10567091

Version No: 2.0

**Input Set:****Output Set:****Started:** 2008-09-25 12:59:17.733**Finished:** 2008-09-25 12:59:22.458**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 725 ms**Total Warnings:** 42**Total Errors:** 0**No. of SeqIDs Defined:** 54**Actual SeqID Count:** 54

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)

**Input Set:**

**Output Set:**

**Started:** 2008-09-25 12:59:17.733  
**Finished:** 2008-09-25 12:59:22.458  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 725 ms  
**Total Warnings:** 42  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 54  
**Actual SeqID Count:** 54

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (35)
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W 402	Undefined organism found in <213> in SEQ ID (40)

# SEQUENCE LISTING

<110> GRIESBECK, OLIVER  
HEIM, NICOLA

<120> NOVEL GENETICALLY ENCODED BIOINDICATORS OF CALCIUM-IONS

<130> 085449-0185

<140> 10567091

<141> 2008-09-25

<150> PCT/EP2004/008739

<151> 2004-08-04

<150> EP 03016691.2

<151> 2003-08-04

<160> 54

<170> PatentIn version 3.3

<210> 1

<211> 1863

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

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tacctgagca ccagtcgcg cctgagcaaa gaccccaacg agaagcgcg tcacatggtc	660
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<210> 2

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	Gly
			20					25						30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys  
225 230 235 240

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr  
245 250 255

Lys	Glu	Leu	Gly	Thr	Val	Met	Arg	Met	Leu	Gly	Gln	Asn	Pro	Thr	Lys	260	265	270
Glu	Glu	Leu	Asp	Ala	Ile	Ile	Glu	Glu	Val	Asp	Glu	Asp	Gly	Ser	Gly	275	280	285
Thr	Ile	Asp	Phe	Glu	Glu	Phe	Leu	Val	Met	Met	Val	Arg	Gln	Met	Lys	290	295	300
Glu	Asp	Ala	Lys	Gly	Lys	Ser	Glu	Glu	Glu	Leu	Ala	Asn	Cys	Phe	Arg	305	310	315
Ile	Phe	Asp	Lys	Asn	Ala	Asp	Gly	Phe	Ile	Asp	Ile	Glu	Glu	Leu	Gly	325	330	335
Glu	Ile	Leu	Arg	Ala	Thr	Gly	Glu	His	Val	Ile	Glu	Glu	Asp	Ile	Glu	340	345	350
Asp	Leu	Met	Lys	Asp	Ser	Asp	Lys	Asn	Asn	Asp	Gly	Arg	Ile	Asp	Phe	355	360	365
Asp	Glu	Phe	Leu	Lys	Met	Met	Glu	Gly	Val	Gln	Glu	Leu	Met	Val	Ser	370	375	380
Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	385	390	395
Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	405	410	415
Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	420	425	430
Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Gly	Tyr	435	440	445
Gly	Leu	Met	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg	Gln	His	Asp	450	455	460
Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	465	470	475
																		480

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe  
485 490 495

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe  
500 505 510

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn  
515 520 525

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys  
530 535 540

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu  
545 550 555 560

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu  
565 570 575

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp  
580 585 590

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala  
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Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
610 615 620

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<211> 1902

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

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ggcaagctga ccttgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca cctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggetacg tccaggagcg taccatcttc	300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg	360



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gaccactacc	agcagaacac	ccccatcggc	gacggccccg	tgctgctgcc	cgacaaccac	600
tacctgagca	cccagtcgcg	cctgagcaaa	gaccccaacg	agaagcgcga	tcacatggtc	660
ctgctggagt	togtgaccgc	cgcccgcgat	ctaattggatg	acatctacaa	ggctgcggta	720
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gaggacgaca	tcgaggaact	catgaaggac	ggagacaaga	acaacgacgg	ccgcatcgac	1140
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gagctgttca	ccgggggtgg	gcccattctg	gtcgagctgg	acggcgacgt	aaacggccac	1260
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accccatcg	gcgacggccc	cgtgctgctg	cccgacaacc	actacctgag	ctaccagtcc	1800
gcctgagca	aagaccccaa	cgagaagcgc	gatcacatgg	tctgctgga	gttcgtgacc	1860
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<210> 4

<211> 633

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
polypeptide

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			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75				80	

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105						110	

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				

Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155				160	

Gly	Ile	Lys	Ala	His	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
			165						170					175	

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
			180						185				190		

Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
			195				200						205		

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Arg Met Leu Met Asp Asp Ile Tyr Lys Ala Ala Val  
225 230 235 240

Glu Gln Leu Thr Glu Glu Gln Lys Asn Glu Phe Lys Ala Ala Phe Asp  
245 250 255

Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile Ser Thr Lys Glu Leu  
260 265 270

Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro Thr Pro Glu Glu Leu  
275 280 285

Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly Ser Gly Thr Val Asp  
290 295 300

Phe Asp Glu Phe Leu Val Met Met Val Arg Cys Met Lys Asp Asp Ser  
305 310 315 320

Lys Gly Lys Ser Glu Glu Glu Leu Ser Asp Leu Phe Arg Met Phe Asp  
325 330 335

Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu Leu Lys Ile Met Leu  
340 345 350

Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp Ile Glu Glu Leu Met  
355 360 365

Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile Asp Tyr Asp Glu Phe  
370 375 380

Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met Val Ser Lys Gly Glu  
385 390 395 400

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp  
405 410 415

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala  
420 425 430

Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu
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Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg	Gln	His	Asp	Phe	Phe	Lys
465				470				475				480			
Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys
				485				490				495			
Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp
				500				505				510			
Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp
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Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn
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Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala	Asn	Phe
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Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His
				565				570				575			
Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp
580				585				590							
Asn	His	Tyr	Leu	Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu
595				600				605							
Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile
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Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys							
625				630											

<210> 5

<211> 1863

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

<400> 5

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ggcaagctga cctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca cctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag	240
cagcacgact ttttcaagtc cgccatgccc gaaggetacg tccaggagcg taccatcttc	300
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ggcatcaagg ccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac	600
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ctgctggagt tcgtgaccgc cgcccgcatg ctcagcgagg agatgattgc tgagttcaaa	720
gctgcctttg acatgtttga tgcggacggt ggtggggaca tcagcaccaa ggagttgggc	780
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